

## SEQUENCE LISTING

5 <110> SunGene GmbH & Co. KGaA

10 <120> Process for the preparation of  $\beta$ -carotenoids

<130> PF 54755

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20 <170> PatentIn version 3.1

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 35 40 45  
 25 Leu Arg Ser Arg Arg Lys Pro Ser Phe Thr Val Cys Phe Val Leu Glu  
 50 55 60  
 30 Asp Glu Lys Leu Lys Pro Gln Phe Asp Asp Glu Ala Glu Asp Phe Glu  
 65 70 75 80  
 35 Lys Lys Ile Glu Glu Gln Ile Leu Ala Thr Arg Leu Ala Glu Lys Leu  
 85 90 95  
 40 Ala Arg Lys Lys Ser Glu Arg Phe Thr Tyr Leu Val Ala Ala Ile Met  
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 45 Phe Ser Trp Gln Met Glu Gly Gly Glu Val Pro Val Thr Glu Met Leu  
 130 135 140  
 50 Gly Thr Phe Ala Leu Ser Val Gly Ala Ala Val Gly Met Glu Phe Trp  
 145 150 155 160

14

Ala Arg Trp Ala His Lys Ala Leu Trp His Ala Ser Leu Trp His Met  
165 170 175

5 His Glu Ser His His Lys Pro Arg Glu Gly Pro Phe Glu Leu Asn Asp  
180 185 190

10 Val Phe Ala Ile Thr Asn Ala Val Pro Ala Ile Ala Leu Leu Asn Tyr  
195 200 205

15 Gly Phe Phe His Lys Gly Leu Ile Ala Gly Leu Cys Phe Gly Ala Gly  
210 215 220

20 Leu Gly Ile Thr Val Phe Gly Met Ala Tyr Met Phe Val His Asp Gly  
225 230 235 240

25 Leu Val His Lys Arg Phe Pro Val Gly Pro Val Ala Asn Val Pro Tyr  
245 250 255

30 Leu Arg Lys Val Ala Ala Ala His Ser Leu His His Ser Glu Lys Phe  
260 265 270

35 Asn Gly Val Pro Tyr Gly Leu Phe Phe Gly Pro Lys Glu Leu Glu Glu  
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10 gatacaaggc gtgactggat atttctctct cgttcctaac aacagcaacg aagaagaaaa 120

agaatcatta ctaacaatca atg agt atg aga gct gga cac atg acg gca aca 173

Met Ser Met Arg Ala Gly His Met Thr Ala Thr

1 5 10

15

atg gcg gct ttt aca tgc cct agg ttt atg act agc atc aga tac acg 221

Met Ala Ala Phe Thr Cys Pro Arg Phe Met Thr Ser Ile Arg Tyr Thr

15 20 25

20 aag caa att aag tgc aac gct gct aaa agc cag cta gtc gtt aaa caa 269

Lys Gln Ile Lys Cys Asn Ala Ala Lys Ser Gln Leu Val Val Lys Gln

30 35 40

gag att gag gag gaa gaa gat tat gtg aaa gcc ggt gga tcg gag ctg 317

25 Glu Ile Glu Glu Glu Glu Asp Tyr Val Lys Ala Gly Gly Ser Glu Leu

45 50 55

ctt ttt gtt caa atg caa cag aat aag tcc atg gat gca cag tct agc 365

Leu Phe Val Gln Met Gln Gln Asn Lys Ser Met Asp Ala Gln Ser Ser

30 60 65 70 75

cta tcc caa aag ctc cca agg gta cca ata gga gga gga gga gac agt 413

Leu Ser Gln Lys Leu Pro Arg Val Pro Ile Gly Gly Gly Gly Asp Ser

80 85 90

35

aac tgt ata ctg gat ttg gtt gta att ggt tgt ggt cct gct ggc ctt 461

Asn Cys Ile Leu Asp Leu Val Val Ile Gly Cys Gly Pro Ala Gly Leu

95 100 105

40 gct ctt gct gga gaa tca gcc aag cta ggc ttg aat gtc gca ctt atc 509

Ala Leu Ala Gly Glu Ser Ala Lys Leu Gly Leu Asn Val Ala Leu Ile

110 115 120

ggc cct gat ctt cct ttt aca aat aac tat ggt gtt tgg gag gat gaa 557

45 Gly Pro Asp Leu Pro Phe Thr Asn Asn Tyr Gly Val Trp Glu Asp Glu

125 130 135

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Phe Ile Gly Leu Gly Leu Glu Gly Cys Ile Glu His Val Trp Arg Asp

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Thr Val Val Tyr Leu Asp Asp Asn Asp Pro Ile Leu Ile Gly Arg Ala

160 165 170

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5	tgc atg gag tca ggc gtt tca tat ctg agc tcc aaa gtg gaa cgg att	749
	Cys Met Glu Ser Gly Val Ser Tyr Leu Ser Ser Lys Val Glu Arg Ile	
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	Thr Glu Ala Pro Asn Gly Leu Ser Leu Ile Glu Cys Glu Gly Asn Ile	
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	220 225 230 235	
20	aaa ctt ttg cag tat gaa ctt ggc ggt ccc cgt gtt tgc gtt caa aca	893
	Lys Leu Leu Gln Tyr Glu Leu Gly Gly Pro Arg Val Cys Val Gln Thr	
	240 245 250	
25	gct tat ggt ata gag gtt gag gtt gaa agc ata ccc tat gat cca agc	941
	Ala Tyr Gly Ile Glu Val Glu Val Glu Ser Ile Pro Tyr Asp Pro Ser	
	255 260 265	
30	cta atg gtt ttc atg gat tat aga gac tac acc aaa cat aaa tct caa	989
	Leu Met Val Phe Met Asp Tyr Arg Asp Tyr Thr Lys His Lys Ser Gln	
	270 275 280	
35	tca cta gaa gca caa tat cca aca ttt ttg tat gtc atg cca atg tct	1037
	Ser Leu Glu Ala Gln Tyr Pro Thr Phe Leu Tyr Val Met Pro Met Ser	
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	Pro Thr Lys Val Phe Phe Glu Glu Thr Cys Leu Ala Ser Lys Glu Ala	
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	Met Gly Ile Arg Ile Thr Lys Thr Tyr Glu Glu Glu Trp Ser Tyr Ile	
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55	cca gta ggt gga tcc tta cca aat acc gag caa aag aac ctt gca ttt	1229
	Pro Val Gly Gly Ser Leu Pro Asn Thr Glu Gln Lys Asn Leu Ala Phe	
	350 355 360	
60	ggg gct gct gct agc atg gtg cat cca gcc aca gga tat tcg gtt gta	1277
	Gly Ala Ala Ala Ser Met Val His Pro Ala Thr Gly Tyr Ser Val Val	
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65	aga tca ctg tca gaa gct cct aat tat gca gca gta att gca aag att	1325



## 17

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	Leu	Gly	Lys	Gly	Asn	Ser	Lys	Gln	Met	Leu	Asp	His	Gly	Arg	Tyr	Thr	
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10	acc	aac	atc	tca	aag	caa	gct	tgg	gaa	aca	ctt	tgg	ccc	ctt	gaa	agg	1421
	Thr	Asn	Ile	Ser	Lys	Gln	Ala	Trp	Glu	Thr	Leu	Trp	Pro	Leu	Glu	Arg	
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15	aaa	aga	cag	aga	gca	ttc	ttt	ctc	ttt	gga	tta	gca	ctg	att	gtc	cag	1469
	Lys	Arg	Gln	Arg	Ala	Phe	Phe	Leu	Phe	Gly	Leu	Ala	Leu	Ile	Val	Gln	
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	Met	Asp	Ile	Glu	Gly	Thr	Arg	Thr	Phe	Phe	Arg	Thr	Phe	Phe	Arg	Leu	
					445				450					455			
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	Pro	Thr	Trp	Met	Trp	Trp	Gly	Phe	Leu	Gly	Ser	Ser	Leu	Ser	Ser	Thr	
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25	gac	ttg	ata	ata	ttt	gcg	ttt	tac	atg	ttt	atc	ata	gca	ccg	cat	agc	1613
	Asp	Leu	Ile	Ile	Phe	Ala	Phe	Tyr	Met	Phe	Ile	Ile	Ala	Pro	His	Ser	
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	Leu	Arg	Met	Gly	Leu	Val	Arg	His	Leu	Leu	Ser	Asp	Pro	Thr	Gly	Gly	
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35	aca	atg	tta	aaa	gcg	tat	ctc	acg	ata	taa	ataactctag	tcgcgatcag					1711
	Thr	Met	Leu	Lys	Ala	Tyr	Leu	Thr	Ile								
					510				515								
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10																	
	Glu	Asp	Tyr	Val	Lys	Ala	Gly	Gly	Ser	Glu	Leu	Leu	Phe	Val	Gln	Met	
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	Gln	Gln	Asn	Lys	Ser	Met	Asp	Ala	Gln	Ser	Ser	Leu	Ser	Gln	Lys	Leu	
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	Ser	Ala	Lys	Leu	Gly	Leu	Asn	Val	Ala	Leu	Ile	Gly	Pro	Asp	Leu	Pro	
			115					120					125				
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	Phe	Thr	Asn	Asn	Tyr	Gly	Val	Trp	Glu	Asp	Glu	Phe	Ile	Gly	Leu	Gly	
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	Leu	Glu	Gly	Cys	Ile	Glu	His	Val	Trp	Arg	Asp	Thr	Val	Val	Tyr	Leu	
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5	Glu	Leu	Gly	Gly	Pro	Arg	Val	Cys	Val	Gln	Thr	Ala	Tyr	Gly	Ile	Glu	
					245					250					255		
10	Val	Glu	Val	Glu	Ser	Ile	Pro	Tyr	Asp	Pro	Ser	Leu	Met	Val	Phe	Met	
				260					265					270			
15	Asp	Tyr	Arg	Asp	Tyr	Thr	Lys	His	Lys	Ser	Gln	Ser	Leu	Glu	Ala	Gln	
			275					280						285			
20	Tyr	Pro	Thr	Phe	Leu	Tyr	Val	Met	Pro	Met	Ser	Pro	Thr	Lys	Val	Phe	
		290					295					300					
25	Phe	Glu	Glu	Thr	Cys	Leu	Ala	Ser	Lys	Glu	Ala	Met	Pro	Phe	Glu	Leu	
	305					310					315					320	
30	Leu	Lys	Thr	Lys	Leu	Met	Ser	Arg	Leu	Lys	Thr	Met	Gly	Ile	Arg	Ile	
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35	Thr	Lys	Thr	Tyr	Glu	Glu	Glu	Trp	Ser	Tyr	Ile	Pro	Val	Gly	Gly	Ser	
				340					345					350			
40	Leu	Pro	Asn	Thr	Glu	Gln	Lys	Asn	Leu	Ala	Phe	Gly	Ala	Ala	Ala	Ser	
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45	Met	Val	His	Pro	Ala	Thr	Gly	Tyr	Ser	Val	Val	Arg	Ser	Leu	Ser	Glu	
		370					375					380					
50	Ala	Pro	Asn	Tyr	Ala	Ala	Val	Ile	Ala	Lys	Ile	Leu	Gly	Lys	Gly	Asn	
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55	Ser	Lys	Gln	Met	Leu	Asp	His	Gly	Arg	Tyr	Thr	Thr	Asn	Ile	Ser	Lys	
					405					410					415		
60	Gln	Ala	Trp	Glu	Thr	Leu	Trp	Pro	Leu	Glu	Arg	Lys	Arg	Gln	Arg	Ala	
				420					425					430			
65	Phe	Phe	Leu	Phe	Gly	Leu	Ala	Leu	Ile	Val	Gln	Met	Asp	Ile	Glu	Gly	
			435					440					445				

Thr Arg Thr Phe Phe Arg Thr Phe Phe Arg Leu Pro Thr Trp Met Trp  
 450 455 460  
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Trp Gly Phe Leu Gly Ser Ser Leu Ser Ser Thr Asp Leu Ile Ile Phe  
 465 470 475 480  
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Ala Phe Tyr Met Phe Ile Ile Ala Pro His Ser Leu Arg Met Gly Leu  
 485 490 495  
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Val Arg His Leu Leu Ser Asp Pro Thr Gly Gly Thr Met Leu Lys Ala  
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Tyr Leu Thr Ile  
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25 <211> 358

<212> DNA

<213> Tagetes erecta

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<220>

35 <221> Sense promoter

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<223>

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 tggagtttaa ttaaaataaa gagaagagaa agattaagag ggtgatgggg atattaaaga 180  
 50 cggccaatat agtgatgcca cgtagaaaaa ggtaagtga aacatacaac gtggctttaa 240  
 aagatggctt ggctgctaact caactcaact caactcatat cctatccatt caaattcaat 300  
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 30 ggcggctttt acatgcccta ggtttatgac tagcatcaga tacacgaagc aaattaagt 240  
 caacgctgct aaaagccagc tagtcgttaa acaagagatt gaggaggaag aagattatgt 300  
 gaaagccggt ggatcggagc tgctttttgt tcaaatgcaa cagaataagt ccatggatgc 360  
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 40 <210> 11  
 <211> 446  
 45 <212> DNA  
 <213> *Tagetes erecta*  
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&lt;223&gt;

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&lt;400&gt; 11

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aaacagatac aaggcgtgac tggatatttc tctctcggtc ctaacaacag caacgaagaa 120

gaaaaagaat cattactaac aatcaatgag tatgagagct ggacacatga cggcaacaat 180

15

ggcggtttt acatgcccta gggttatgac tagcatcaga tacacgaagc aaattaagtg 240

caacgctgct aaaagccagc tagtcgttaa acaagagatt gaggaggaag aagattatgt 300

gaaagccggt ggatcggagc tgctttttgt tcaaagtcaa cagaataagt ccatggatgc 360

20

acagtctagc ctatcccaaa agctcccaag ggtaccaata ggaggaggag gagacagtaa 420

ctgtatactg gatttggttg gatcct 446

25

&lt;210&gt; 12

&lt;211&gt; 393

&lt;212&gt; DNA

30

<213> *Tagetes erecta*

35

&lt;220&gt;

&lt;221&gt; Sense fragment

&lt;222&gt; (1)..(393)

40

&lt;223&gt;

45

&lt;400&gt; 12

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aactgacttg ataattttg cgttttacat gtttatcata gcaccgcata gcctgagaat 180

gggtctggtt agacatttgc tttctgaccc gacaggagga acaatgttaa aagcgtatct 240

cacgatataa ataactctag tcgcgatcag tttagattat aggcacatct tgcatatata 300

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 tatatatgta taaaccttat gtgtgctgta tccttacatc aacacagtca ttaattgtat 360  
 40 ttcttggggg aatgctgatg aagtattttc tggatcc 397  
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 <212> DNA  
 <213> Tagetes erecta  
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 <220>

&lt;221&gt; Sense promoter

&lt;222&gt; (1)..(358)

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&lt;400&gt; 14

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 cggccaatat agtgatgcca cgtagaaaaa ggtaagtga aacatacaac gtggctttaa 240  
 aagatggctt ggctgctaact caactcaact caactcatat cctatccatt caaattcaat 300  
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&lt;210&gt; 15

25 &lt;211&gt; 361

&lt;212&gt; DNA

30 &lt;213&gt; Tagetes erecta

&lt;220&gt;

35 &lt;221&gt; Antisense promoter

&lt;222&gt; (1)..(361)

40 &lt;223&gt;

&lt;400&gt; 15

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 taggctttgt tgtgagaatg ttgagaaaga ggtttgacaa atcgggtgtt gaatgagggt 120  
 aaatggagtt taattaaaat aaagagaaga gaaagattaa gagggtgatg gggatattaa 180  
 50 agacggccaa tatagtgatg ccacgtagaa aaaggtaagt gaaaacatac aacgtggctt 240  
 taaaagatgg cttggctgct aatcaactca actcaactca taccctatcc attcaaattc 300  
 aattcaattc tattgaatgc aaagcaaagc aaagcaaagg ttgtttgttg ttgttggatc 360



c

361

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 10 <213> *Tagetes erecta*

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30 att gct gtc cct tgt agc tca aga cca ttt ggc tta ggt cga atg cgg 96  
 Ile Ala Val Pro Cys Ser Ser Arg Pro Phe Gly Leu Gly Arg Met Arg  
 20 25 30

35 tta ctt ggt cat aaa ccc aca acc ata act tgt cac ttc ccc ttt tct 144  
 Leu Leu Gly His Lys Pro Thr Thr Ile Thr Cys His Phe Pro Phe Ser  
 35 40 45

40 ttt tct atc aaa tca ttt acc cca att gtt agg ggc aga aga tgt act 192  
 Phe Ser Ile Lys Ser Phe Thr Pro Ile Val Arg Gly Arg Arg Cys Thr  
 50 55 60

45 gtt tgt ttt gtt gcc ggt ggc gac agt aat agt aac agt aat aat aat 240  
 Val Cys Phe Val Ala Gly Gly Asp Ser Asn Ser Asn Ser Asn Asn Asn  
 65 70 75 80

agt gac agt aat agt aat aat ccg ggt ctg gat tta aac ccg gcg gtt 288  
 Ser Asp Ser Asn Ser Asn Asn Pro Gly Leu Asp Leu Asn Pro Ala Val  
 85 90 95

50 atg aac cgt aac cgt ttg gtt gaa gaa aaa atg gag agg tcg ac 332  
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 20  
 Leu Leu Gly His Lys Pro Thr Thr Ile Thr Cys His Phe Pro Phe Ser  
 35 40 45  
 25  
 Phe Ser Ile Lys Ser Phe Thr Pro Ile Val Arg Gly Arg Arg Cys Thr  
 50 55 60  
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 Val Cys Phe Val Ala Gly Gly Asp Ser Asn Ser Asn Ser Asn Asn Asn  
 65 70 75 80  
 35  
 Ser Asp Ser Asn Ser Asn Asn Pro Gly Leu Asp Leu Asn Pro Ala Val  
 85 90 95  
 40  
 Met Asn Arg Asn Arg Leu Val Glu Glu Lys Met Glu Arg Ser  
 100 105 110  
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<223>  $\beta$ -Hydroxylase sense fragment

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&lt;400&gt; 18

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10

tgtagctcaa gaccatttgg cttaggtcga atgcgggttac ttggtcataa acccacaacc 120

ataacttgtc acttcccctt ttctttttct atcaaatcat ttacccaat tgtaggggc 180

15

agaagatgta ctgtttgttt tggtgccggg ggcgacagta atagtaacag taataataat 240

agtgcagta atagtaataa tccgggtctg gatttaaacc cggcggttat gaaccgtaac 300

cgtttggttg aagaaaaaat ggagaggctg ac 332

20

&lt;210&gt; 19

&lt;211&gt; 332

25

&lt;212&gt; DNA

<213> *Tagetes erecta*

30

&lt;220&gt;

&lt;221&gt; misc\_feature

35

&lt;222&gt; (1)..(332)

<223>  $\beta$ -Hydroxylase antisense fragment

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&lt;400&gt; 19

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ttgtagctca agaccatttg gcttaggtcg aatgcgggta ttggtcata aaccacaac 120

45

cataacttgt cacttcccct ttctttttt tatcaaatca ttaccccaa ttgtagggg 180

cagaagatgt actgtttgtt ttgttgccgg tggcgacagt aatagtaaca gtaataataa 240

50

tagtgacagt aatagtaata atccgggtct ggatttaaacc ccggcggtta tgaaccgtaa 300

ccgtttggtt gaagaaaaaa tggagaggat cc 332

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15 <222> (1)..(19)  
<223>

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<400> 20  
tgccaaagta actctttat

19

25

<210> 21  
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30 <212> DNA  
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35

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40 <222> (1)..(19)  
<223>

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<400> 21  
agggtgcatga ccaagtaac

19

50

<210> 22  
<211> 1033

&lt;212&gt; DNA

<213> *Lycopersicon esculentum*

5

&lt;220&gt;

&lt;221&gt; Promoter

10

&lt;222&gt; (1)..(1033)

&lt;223&gt;

15

&lt;400&gt; 22

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20	aagaaggcaa agtagagcaa gcaagcaagc aaagcatttt tcttatttta tattttgttg	120
	cggattccac caccacttg aaaaattgac atgtcacaat gatttcgtat cctagtcttt	180
25	tattatttaa cactctcaca atcccattac tctacacctc tttcattaag tcaacacacg	240
	gttttcaaaa atccactacc ctcccaccac ctagaatctt ttgttaccta ccaacaccct	300
	cctttgttct ctttatatat tgggtccaact aaatcaataa gggaaagcat ccttttggtt	360
30	ggaggaattg ctttcattct cactctttgt gtgttgatca atggactagc taataacaag	420
	ttctctctct atatatttca aaagaatgga acagaaacat aaacgaaaga cagagtacct	480
35	gatgttgatg attcattgtc tgtctggagc tcccaaatgc cttttatgct tacatattca	540
	taaccaacaa cggctattaa ttataaacca aaaacacgaa ataagtttgt agcaaagtga	600
	aattaggaat cttggagatg gatccattag tagtaggata ataggatatg atggaatttg	660
40	gttggggaac agtgataact tacgcttgct tccggcgccg ggaaagttgg aaaacctaca	720
	aagtacagaa atggatctgg gccttgaagt gggcttttta ttaaagaaaa aaatacatct	780
45	cggttatcaa tcaccatctt cttctatcta caaattaaag aaggtaacaa cagaacgtgg	840
	tggatcatgt ggtaggcat taattatttg ctttgtttcg ccgttttggt aacacacaga	900
	cacagttccg gtaagagctt ttgcagccac tctttatagt tatttagaat tggcgatcga	960
50	atcaatctca ctccctccct cccttaagtc ttgttgaatc tgctgaattg ttttataaag	1020
	agttactttg gca	1033

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<211> 18

5 <212> DNA

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15 <222> (1)..(18)

<223>

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25 <210> 24

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30 <213> Synthetic sequence

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10 <222> (1)..(28)

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20 <210> 26

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25 <213> Synthetic sequence

30 <220>

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45 <211> 34

<212> DNA

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5 <223>

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10 atcaacggac atcgacttaa cggcgtttgt aaac 34

<210> 28

15 <211> 25

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<220>

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30

<400> 28

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40 <212> DNA

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45

<220>

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50 <222> (1)..(23)

<223>



26

<210> 32  
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40 <223>  
45 <400> 33  
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50  
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29

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20 <211> 28

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25 <213> Synthetic sequence

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45 <211> 25

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25

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30      <210> 40

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40      <220>

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45      <222> (1)..(23)

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25 <210> 42  
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20 <211> 26

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<220>

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15 <211> 28

<212> DNA

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<400> 46

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<223>



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10      <210> 48  
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30      <210> 49  
    <211> 28  
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22

23